

Sequence Listing

<110> ASHKENAZI, AVI J
 BOTSTEIN, DAVID
 DODGE, KELLY H.
 GURNEY, AUSTIN L.
 KIM, KYUNG JIN
 LAWRENCE, DAVID A.
 PITTI, ROBERT
 ROY, MARGARET A
 TUMAS, DANIEL B
 WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met	Arg	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Leu	Leu	Cys	Leu	Val
1				5					10					15

Leu	Ala	Leu	Pro	Ala	Leu	Leu	Pro	Val	Pro	Ala	Val	Arg	Gly	Val
				20					25					30

Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
				35					40					45

Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
				50					55					60

Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
				65					70					75

Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
				80					85					90

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	95	100	105
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	110	115	120
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	125	130	135
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	140	145	150
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	155	160	165
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	170	175	180
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	185	190	195
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	200	205	210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	215	220	225
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	230	235	240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	245	250	255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	260	265	270
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	275	280	285
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	290	295	300

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggc caggcacagc 50
agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggc aggcctgtcg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350
acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaac cgtgcctgcc gctgccgcac 450
cggtctcttc gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac 500
ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc cccagggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggtctcccc 700
ctcagcacca gggtagcagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcggggcgc 850
gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900
gcaggacggg gcgctgctgg tgcggctgct gcaggcgtg cgcgtggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttccct ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

<400> 3
gccgagacag cccacgacg tgtggcccg gtccaccg cactacacg 50

cagttctgga antaactgga gcncctgccgc tactgnaacg tcctctgngg 100

ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgect 150

gccgctgccg caccggcttc ttcgcgcacg ctggtttctg cttggagcac 200

gcatcgtgtc cacctggtgc cggcgtgatt gcccgggca ccccagcca 250

gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300

tccagctcag agcagtgcc accccaccgc aactgcacgg ccctgggcct 350

ggccctcaat gtgccaggct ctctctcca tgacacctg tgcaccagct 400

gcactggctt cccctcagc accagggtac caggagctga ggagtgtgag 450

cgtgcgctca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag cccacgacg tgtggcccg gtccaccg cactacacg 50

cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag cccacgacg tgtggcccgt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gcnctgcag caccggnttc ttcgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncgcgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgctgcc gcaccggctt cttegcgcac gctggtttct gcttggagca 150

cgcacgtgt ccacctggtg cggcgtgat tccccgggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gaggggcccc caggagtggg ggccggagggt gtggcagggg tcaggttgct 50
gggtcccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctggt 100
cttccctcct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
gccccccagg cacctttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttctcccat gacaccctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcatcgtgtc cacctgggtgc cggcgtgatt gccccgggca cccccagcca 50
gaacacgcag gcctagccgt gccccccagg cacctttctca gccagcagct 100
ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150
gccctcaatg tgccaggctc ttctcccat gacaccctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgcnc encaggcacc ttctcagcca gcagttccag ctcagagcag 50

tgccagcccc accgcaactg cacggccctg ggcttgcccc tcaatgtgcc 100
 aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150
 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
 tttgtggctt tccaggacat ctccat 226

<210> 10
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1-283
 <223> Unknown organism

<220>
 <221> unsure
 <222> 27, 64, 140
 <223> unknown base

<400> 10
 cttgtccacc tgggtgccgc gtgattnecc gggcaccccc agccagaaca 50
 cgcagtgcc a gcntcccc caggcacctt ctcagccage agctccagct 100
 cagagcagtg ccagccccac cgcaactgca acgccttggc ctggccctca 150
 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 ttccccctca gcaccagggc accaggagct gaggagtgtg agcgtgccgt 250
 catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
 <211> 21
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown organism

<400> 11
 cacgctgggt tctgcttgga g 21

<210> 12
 <211> 22
 <212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

cttcttcgcg cacgctg 17

<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

[illegible]

<400> 17																
Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu		
1				5					10					15		
Leu	Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr		
				20					25					30		
Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr		
				35					40					45		
Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly		
				50					55					60		
Gln	His	Ala	Lys	Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys		
				65					70					75		
Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val		
				80					85					90		
Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val		
				95					100					105		
Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys		
				110					115					120		
Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg		
				125					130					135		
Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala		
				140					145					150		
Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala		
				155					160					165		
Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg		
				170					175					180		
Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser		
				185					190					195		
Arg	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala		
				200					205					210		

Pro Gly Ala Val	His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln	215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val Asn Cys Val Ile Met Thr	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu	425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro	440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys Pro Ser	455	460	

<210> 18
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	1	5	10	15
Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	20	25	30	
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	35	40	45	
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	50	55	60	
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	65	70	75	
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	80	85	90	
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	95	100	105	
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	110	115	120	
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	125	130	135	
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	140	145	150	
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	155	160	165	
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	170	175	180	
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	185	190	195	
Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	200	205	210	
Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	215	220	225	

